Resource Summary Report

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Parsnp

RRID:SCR_024153
Type: Tool

Proper Citation

Parsnp (RRID:SCR_024153)

Resource Information

URL: https://harvest.readthedocs.io/en/latest/content/parsnp.html

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Description: Software to align the core genome of hundreds to thousands of bacterial genomes. Input can be both draft assemblies and finished genomes, and output includes variant (SNP) calls, core genome phylogeny and multi-alignments. Parsnp leverages contextual information provided by multi-alignments surrounding SNP sites for filtration/cleaning, in addition to existing tools for recombination detection/filtration and phylogenetic reconstruction.

Synonyms: parsnp

Resource Type: software toolkit, software resource, software library

Defining Citation: PMID:25410596

Keywords: align core genome, bacterial genomes,

Funding:

Availability: Free, Available for download, Freely available,

Resource Name: Parsnp

Resource ID: SCR_024153

Alternate IDs: OMICS_21461

Alternate URLs: https://sources.debian.org/src/parsnp/, https://github.com/marbl/parsnp

Record Creation Time: 20230824T050212+0000

Record Last Update: 20250417T065751+0000

Ratings and Alerts

No rating or validation information has been found for Parsnp.

No alerts have been found for Parsnp.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 26 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Meijs AP, et al. (2024) Human carriage of ESBL/pAmpC-producing Escherichia coli and Klebsiella pneumoniae in relation to the consumption of raw or undercooked vegetables, fruits, and fresh herbs. Microbiology spectrum, 12(2), e0284923.

Rhoads DD, et al. (2024) Molecular Genomic Analyses of Enterococcus cecorum from Sepsis Outbreaks in Broilers. Microorganisms, 12(2).

Jiang Y, et al. (2024) Persistent Colonization of Ciprofloxacin-Resistant and Extended-Spectrum ?-Lactamase (ESBL)-Producing Salmonella enterica Serovar Kentucky ST198 in a Patient with Inflammatory Bowel Disease. Infection and drug resistance, 17, 1459.

Ge Q, et al. (2024) Detection of antimicrobial resistance in Glaesserella parasuis in South China using whole-genome sequencing. Frontiers in microbiology, 15, 1532743.

Mattioni Marchetti V, et al. (2024) Enterobacter asburiae ST229: an emerging carbapenemases producer. Scientific reports, 14(1), 6220.

Eddoubaji Y, et al. (2024) A new in vivo model of intestinal colonization using Zophobas morio larvae: testing hyperepidemic ESBL- and carbapenemase-producing Escherichia coli clones. Frontiers in microbiology, 15, 1381051.

Cave R, et al. (2024) Expansion of pneumococcal serotype 23F and 14 lineages with genotypic changes in capsule polysaccharide locus and virulence gene profiles post introduction of pneumococcal conjugate vaccine in Blantyre, Malawi. Microbial genomics,

10(6).

Gong X, et al. (2024) Genomic insight into the diversity of Glaesserella parasuis isolates from 19 countries. mSphere, 9(9), e0023124.

Kille B, et al. (2024) Parsnp 2.0: scalable core-genome alignment for massive microbial datasets. Bioinformatics (Oxford, England), 40(5).

Chan Y-X, et al. (2024) Genomic investigation of Lactococcus formosensis, Lactococcus garvieae, and Lactococcus petauri reveals differences in species distribution by human and animal sources. Microbiology spectrum, 12(6), e0054124.

Uesaka K, et al. (2024) Deciphering the genomes of motility-deficient mutants of Vibrio alginolyticus 138-2. PeerJ, 12, e17126.

Fang C, et al. (2024) Emergence of Staphylococcus argenteus in pediatrics: Molecular insights from a hospital in East China. Virulence, 15(1), 2396477.

Caméléna F, et al. (2024) Emergence of Extensively Drug-Resistant Neisseria gonorrhoeae, France, 2023. Emerging infectious diseases, 30(9), 1903.

Anbo M, et al. (2023) A bittersweet fate: detection of serotype switching in Pseudomonas aeruginosa. Microbial genomics, 9(1).

Biedrzycka M, et al. (2023) Country-wide expansion of a VIM-1 carbapenemase-producing Klebsiella oxytoca ST145 lineage in Poland, 2009-2019. European journal of clinical microbiology & infectious diseases : official publication of the European Society of Clinical Microbiology, 42(12), 1449.

Zang X, et al. (2023) Evidence of potential Campylobacter jejuni zooanthroponosis in captive macaque populations. Microbial genomics, 9(10).

Xu T, et al. (2022) Frequent convergence of mcr-9 and carbapenemase genes in Enterobacter cloacae complex driven by epidemic plasmids and host incompatibility. Emerging microbes & infections, 11(1), 1959.

Cao H, et al. (2022) Diversity of genomic clusters and CfiA/cfiA alleles in Bacteroides fragilis isolates from human and animals. Anaerobe, 75, 102567.

Ramli SR, et al. (2021) Complete Genome Sequencing of Leptospira interrogans Isolates from Malaysia Reveals Massive Genome Rearrangement but High Conservation of Virulence-Associated Genes. Pathogens (Basel, Switzerland), 10(9).

Snell SB, et al. (2021) Staphylococcus aureus Tolerance and Genomic Response to Photodynamic Inactivation. mSphere, 6(1).